
 WIRE RELEASE (TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Wed Aug 20 09:44:12 1997; MasPar time 12.79 Seconds
 665.067 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-469-637A-2
 Description: (1-401) from US08469637A.pep (1 of 2)
 Perfect Score: 3030
 Sequence: 1 MNKLCCALVFLDISIKWT.....QKLELMIGNQVSKISCL 401

Scoring table: PAM 150
 Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

swiss-prot34
 1:part8 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.313; Variance 81.174; scale 0.595

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

ult	Score	Query Match	Length	ID	Description	Pred. No.
1	405	13.4	461	9	TNR2_HUMAN	1.33e-63
2	375	12.4	474	9	TNR2_MOUSE	9.05e-57
3	303	10.0	277	2	CD40_HUMAN	1.03e-40
4	294	9.7	289	2	CD40_MOUSE	9.50e-39
5	269	8.9	326	10	VT2_MTXVL	2.38e-33
6	265	8.7	415	9	TNRC_MOUSE	1.70e-32
7	260	8.6	325	10	VT2_SEVKA	1.97e-31
8	260	8.6	435	9	TNRC_HUMAN	9.20e-26
9	233	7.7	349	10	VC22_VARV	2.72e-23
10	221	7.3	454	9	TNR1_MOUSE	4.35e-23
11	220	7.3	461	9	TNR1_RAT	4.35e-22
12	215	7.1	416	6	NGFR_CHICK	1.15e-21
13	213	7.0	427	6	NGFR_HUMAN	1.87e-20
14	207	6.8	425	6	NGFR_RAT	1.08e-16
15	188	6.2	323	3	FASA_BOVIN	2.66e-16
16	186	6.1	461	9	TNR1_PIG	9.30e-15
17	178	5.9	595	2	CD30_HUMAN	1.29e-13
18	172	5.7	455	9	TNR1_HUMAN	3.45e-11
19	159	5.2	256	1	41BB_MOUSE	7.67e-09
20	159	5.2	260	2	CD27_HUMAN	1.73e-08
21	146	4.8	271	7	OX40_RAT	
22	144	4.8	272	7	OX40_MOUSE	

RESULT	ID	TNR2_HUMAN	STANDARD:	PRT:	461 AA.
23	141	4.7	277	7	OX40_HUMAN
24	140	4.6	255	1	41BB_HUMAN
25	137	4.5	327	3	FASA_MOUSE
26	134	4.4	250	2	CD27_MOUSE
27	134	4.4	335	3	FASA_HUMAN
28	124	4.1	103	10	VA53_VACCC
29	124	4.1	103	10	VA53_VACCC
30	115	3.8	360	11	YTH9_YEAST
31	110	3.6	535	3	D2_DICDI
32	105	3.5	2813	10	VWF_HUMAN
33	102	3.4	3084	6	LMAI_MOUSE
34	101	3.3	712	4	GFAL_CANAL
35	101	3.3	1122	11	VC3C_YEAST
36	100	3.3	1752	3	DESP_HUMAN
37	99	3.3	2670	11	YAO5_SCHPO
38	96	3.2	431	7	PHOR_SHIDY
39	98	3.2	494	7	PR31_YEAST
40	96	3.2	1104	9	SVY_YEAST
41	96	3.2	1203	10	KXPE_XENLA
42	96	3.2	1356	5	KAB7_YEAST
43	98	3.2	1947	6	PBMC_CAEL
44	96	3.2	3707	7	PGBM_MOUSE
45	97	3.2	4092	3	DYHC_YEAST

ALIGNMENTS

RESULT	ID	TNR2_HUMAN	STANDARD:	PRT:	461 AA.
AC	P20333				
DT	01-FEB-1991 (REL. 17, CREATED)				
DT	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)				
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)				
DE	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR				
DE	BINDING PROTEIN 2) (TbRII) (P80) (TNF-R2) (P75) (CD120B).				
GN	TNFR2 OR TNFR.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:				
CC	EDHERIA: PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 90260639.				
RA	SMITH C.A., DAVIS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERZY R.,				
RA	DOMER S.R., COSMAN D., GOODWIN R.G.,				
RL	SCIENCE 248:1019-1023(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 91045991.				
RA	KOHNO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W.,				
RA	HALE K.K., SOUIRES C.H., THOMPSON R.C., VANNICE J.L.,				
RL	PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).				
RN	[3]				
RP	SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.				
RX	MEDLINE: 90349572.				
RA	HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,				
RL	RINGOLD G.M.,				
RP	PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).				
RN	[4]				
RP	SEQUENCE OF 27-31.				
RX	MEDLINE: 90110215.				
RA	ENGELMANN H., NOVICK D., WALLACH D.,				
RL	J. BIOL. CHEM. 265:1531-1536(1990).				
RN	[5]				
RP	SEQUENCE OF 22-40: 65-69; 136-141; 300-306 AND 346-362.				
RX	MEDLINE: 91056048.				
RA	LOETSCHER H., SCHLAEGEL E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,				
RL	J. BIOL. CHEM. 265:20131-20138(1990).				
RN	[6]				
RP	CHARACTERIZATION.				
RX	MEDLINE: 93016040.				
RA	PENNICA D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M.,				
RL	LIPARI M.T., GOEDDEL D.V.,				

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RL J. BIOL. CHEM. 267:21172-21178(1992).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
CC LEVEL ON THREONINE RESIDUES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M32315; G189186; -.
DR EMBL: M35857; G339752; -.
DR EMBL: M55944; G339758; -.
DR PIR: A35356; A35356.
DR PIR: A36007; A36007.
DR PIR: A36475; A36475.
DR PIR: B35010; B35010.
DR PIR: A23666; A23666.
DR HSSP: P19438; 1TNR.
DR MIM: 191191; -.
DR PROSITE: PS00652; TNFR_NGFR.
DR RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;
KW PHOSPHORYLATION.
FT CHAIN 1 22
FT DOMAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT TRANSMEM 258 287 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 288 461 POTENTIAL.
FT DOMAIN 39 201 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 76 4 X TNFR-CYS.
FT REPEAT 77 118 TNFR-CYS 1.
FT REPEAT 119 162 TNFR-CYS 2.
FT REPEAT 163 201 TNFR-CYS 3.
FT REPEAT 201 253 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 67 75 BY SIMILARITY.
FT DISULFID 75 93 BY SIMILARITY.
FT DISULFID 93 96 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 BY SIMILARITY.
FT CARBOHYD 193 193 POTENTIAL.
FT CONFLICT 141 141 R -> P (IN REF. 3).
FT CONFLICT 141 141 R -> M (IN REF. 1).
FT CONFLICT 196 196 A -> T (IN REF. 3).
FT CONFLICT 363 363
FT SEQUENCE 461 AA: 48316 MW: 0F5D0C44 CRC32;

Query Match 13.48; Score 405; DB 9; Length 461;
st Local Similarity 41.88; Pred. No. 1,33e+63;
atches 69; Conservative 26; Mismatches 59; Indels 11; Gaps 8;

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
RX SEQUENCE FROM N.A.
RX MEDLINE: 91187885.
RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA WONG G.H., CHEN E.Y., GOEDEL D.V.,
RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN (2)
RN SEQUENCE FROM N.A.
RX MEDLINE: 91246168.
RA GOODWIN R.G., ANDERSON D., JERRY R., DAVIS T., BRANNAN C.I.,
RA COPELAND N.G., JENKINS N.A., SMITH C.A.,
RL MOL. CELL. BIOL. 11:3020-3026(1991).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M59378; G202095; -.
DR EMBL: M59378; G202095; -.
DR PIR: B38634; B38634.
DR HSSP: P19438; 1TNR.
DR PROSITE: PS00652; TNFR_NGFR.
DR RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
KW SIGNAL.
FT CHAIN 1 22
FT DOMAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT TRANSMEM 259 288 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 289 474 POTENTIAL.
FT DOMAIN 39 203 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 77 4 X TNFR-CYS.
FT REPEAT 78 119 TNFR-CYS 1.
FT REPEAT 120 164 TNFR-CYS 2.
FT REPEAT 165 203 TNFR-CYS 3.
FT DISULFID 40 54 TNFR-CYS 4.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 68 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 POTENTIAL.
FT CARBOHYD 195 195 POTENTIAL.
FT SEQUENCE 474 AA: 50319 MW: DC32B2B6 CRC32;

Query Match 12.48; Score 375; DB 9; Length 474;
Best Local Similarity 41.58; Pred. No. 9.05e+57;
Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps 7;

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; PRIMATES.
 (1)
 CC SEQUENCE FROM N.A.
 RX MEDLINE: 89356608.
 RA STAMENKOVIC I., CLARK E.A., SEED B.;
 RL EMBO J. 8:1403-1410(1989).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: X60592; G29851.
 DR PIR: S04460; S04460.
 DR MIM: 109535;
 DR PROSITE: PS00652; TNFR_NGFR.
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT CHAIN 1 19
 FT SIGNAL 1 19
 FT DOMAIN 20 277
 FT TRANSMEM 194 215
 FT DOMAIN 216 277
 FT DOMAIN 25 187
 FT REPEAT 25 60
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 FT CARBOHYD 180 180
 SQ SEQUENCE 277 AA; 30619 MW; 3B284411 CRC32;
 Query Match 10.08; Score 303; DB 2; Length 277;
 Best Local Similarity 36.88; Pred. No. 1.03e-40;
 Matches 56; Conservative 21; Mismatches 67; Indels 8; Gaps 7;
 Db 38 csdgcgqgkivsaqctetfctecjpcgeselfdwrethqnhkycdpn-1g1r-vqgkx 95
 QY 41 CDKCPPTGYLKQHCITAKMKTVCAPCPDHYITDSMHTSDC-L--YCSFVCKELQYVKQEC 97
 Db 96 tseadtlctceegwhctseacescvlhrscspgfyvkqialtyvsdtlcepcpvgffsnvs 155
 QY 98 NRTNHNVCCEKRGY-L-EL-EFCLKRRSCPPGFGVQAGTPERNITVCKRCRCPDGFSSNET 154
 Db 156 safekchpwtscetkdlvvgagctnktdivcg 187
 QY 155 SSKAPCRKHTNCSVFGILLTKQGNATHDNICS 186
 LT 4
 CD40_MOUSE STANDARD; PRT; 289 AA.
 P27512;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).
 GN CD40.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 (1)
 CC SEQUENCE FROM N.A.
 RX MEDLINE: 92105763.
 RA TORRES R.M., CLARK E.A.;
 RL J. IMMUNOL. 148:620-626(1992).
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M95181; G332310.
 DR EMBL: A23729; E199442.
 DR PIR: A40566; GOVZML.
 DR HSSP: P19438; ITNR.
 DR PROSITE: PS00652; TNFR_NGFR.
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT CHAIN 1 16
 FT SIGNAL 1 16
 FT DOMAIN 27 186
 FT TRANSMEM 194 215
 FT DOMAIN 216 277
 FT DOMAIN 25 187
 FT REPEAT 25 60
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 FT CARBOHYD 180 180
 SQ SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;
 Query Match 9.7%; Score 294; DB 2; Length 289;
 Best Local Similarity 38.88; Pred. No. 9.50e-39;
 Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;
 Db 38 cdicpgysrlstchlektqchpcdsgefsagwreirchqhrhepn-qglr-vkxag 95
 QY 41 CDKCPPTGYLKQHCITAKMKTVCAPCPDHYITDSMHTSDC-LY--CSFVCKELQYVKQEC 97
 Db 96 taesdvcckegqhtscdceacaghtpcipgfygmataetdvcchpcpvgffsnvs 155
 QY 98 NRTNHNVCCEKRGY-L-EL-EFCLKRRSCPPGFGVQAGTPERNITVCKRCRCPDGFSSNET 154
 Db 156 slfekcypwtscetkdlvvgagctnktdivcg 187
 QY 155 SSKAPCRKHTNCSVFGILLTKQGNATHDNICS 186
 RESULT 5
 ID VT2_MYXVL STANDARD; PRT; 326 AA.
 AC P29825;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS MYXOMA VIRUS (STRAIN LAUSANNE).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXYIRINAE;
 RN LEPORIPVIRUSES.
 (1)
 CC SEQUENCE FROM N.A.
 RX MEDLINE: 91335768.
 RA UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
 RL VIROLOGI 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M95181; G332310.
 DR EMBL: A23729; E199442.
 DR PIR: A40566; GOVZML.
 DR HSSP: P19438; ITNR.
 DR PROSITE: PS00652; TNFR_NGFR.
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT CHAIN 1 16
 FT SIGNAL 1 16
 FT DOMAIN 27 186
 FT TRANSMEM 194 215
 FT DOMAIN 216 277
 FT DOMAIN 25 187
 FT REPEAT 25 60
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 FT CARBOHYD 180 180
 SQ SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;

RA HOWARD M., COCKAYNE D.A.;
 RL J. IMMUNOL. 149:3921-3926(1992).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M83312; G1553059.
 DR EMBL: M84126; G192526.
 DR EMBL: M84129; G192526; JOINED.
 DR EMBL: M94128; G192526; JOINED.
 DR EMBL: M94127; G192526; JOINED.
 DR PIR: A46476; A46476.
 DR HSSP: P19438; ITNR.
 DR PROSITE: PS00652; TNFR_NGFR.
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT CHAIN 1 19
 FT SIGNAL 1 19
 FT DOMAIN 20 289
 FT TRANSMEM 194 215
 FT TRANSMEM 216 289
 FT DOMAIN 25 187
 FT DOMAIN 25 187
 FT REPEAT 25 60
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 SQ SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;
 Query Match 9.7%; Score 294; DB 2; Length 289;
 Best Local Similarity 38.88; Pred. No. 9.50e-39;
 Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;
 Db 38 cdicpgysrlstchlektqchpcdsgefsagwreirchqhrhepn-qglr-vkxag 95
 QY 41 CDKCPPTGYLKQHCITAKMKTVCAPCPDHYITDSMHTSDC-LY--CSFVCKELQYVKQEC 97
 Db 96 taesdvcckegqhtscdceacaghtpcipgfygmataetdvcchpcpvgffsnvs 155
 QY 98 NRTNHNVCCEKRGY-L-EL-EFCLKRRSCPPGFGVQAGTPERNITVCKRCRCPDGFSSNET 154
 Db 156 slfekcypwtscetkdlvvgagctnktdivcg 187
 QY 155 SSKAPCRKHTNCSVFGILLTKQGNATHDNICS 186
 RESULT 5
 ID VT2_MYXVL STANDARD; PRT; 326 AA.
 AC P29825;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS MYXOMA VIRUS (STRAIN LAUSANNE).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXYIRINAE;
 RN LEPORIPVIRUSES.
 (1)
 CC SEQUENCE FROM N.A.
 RX MEDLINE: 91335768.
 RA UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
 RL VIROLOGI 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M95181; G332310.
 DR EMBL: A23729; E199442.
 DR PIR: A40566; GOVZML.
 DR HSSP: P19438; ITNR.
 DR PROSITE: PS00652; TNFR_NGFR.
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT CHAIN 1 16
 FT SIGNAL 1 16
 FT DOMAIN 27 186
 FT TRANSMEM 194 215
 FT DOMAIN 216 277
 FT DOMAIN 25 187
 FT REPEAT 25 60
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 FT CARBOHYD 180 180
 SQ SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;

FT	DISULFID	104	124	BY SIMILARITY.
FT	DISULFID	126	132	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	142	169	BY SIMILARITY.
FT	DISULFID	172	187	BY SIMILARITY.
FT	CARBOHYD	40	40	POTENTIAL.
FT	CARBOHYD	179	179	POTENTIAL.
SO	SEQUENCE	415 AA;	44956 MW; 305DD121 CRC32;	

Query Match	8.7%;	Score 265;	DB 9;	Length 415;
Best Local Similarity 28.9%;				
Matches 54;	Conservative 30;	Mismatches 92;	Indels 11;	Gaps 8;

Db	52	epmhdvccscippggefifavcsrsqdtvcktcphnsynehnhlstcqlcrp.cdvlvgf	110
OY	34	ETSHQLLDCRCPGPTYLKQHCTAKMKITVCAPCPDHYTDSWHTSDECLYCSPYCKE-LQY	92
Db	111	eavpccsdiaercrcqpmgscvylmncvncceerlvlcqpgcaewdeimdtvncv	170
OY	93	VK-OECNTHNRHVECKEGR--YLEIE-FCLNHR-S-CPFGGV-VQAGTPERNIVCK	143
Db	171	pckpghfngntsparcqphtrceiqglveaapqtsydticknppepnamlla11sl	230
OY	144	RCPPGFFSNESSSAPKPKRKHNCVSFGLLLTKGNATHDNDCSGNSESTONCGIDVILCE	203
Db	231	vl1llf 237	
OY	204	EAFRFA 210	

RESULT	7	STANDARD;	PRT;	325 AA.
ID	VT2_SFVKA			
AC	P25943;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).			
GN	T2.			
OS	SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).			
OC	VIRIDAE: DS-DNA ENVELOPED VIRUSES; POXYIRIDAE; CHORDOPOXYIRINAE;			
OC	LEPORIPOVIRUSES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 87321103.			
RA	UPTON C., DELANGE A.M., MCFADDEN G.;			
RA	VIROLOGY. 160:20-30(1987).			
RN	[2]			
RP	FUNCTION.			
RX	MEDLINE: 91207415.			
RA	SMITH C.A., DAVIS T., MIGNALL J.M., DIN W.S., FARRAH T., UPTON C.,			
RA	MCFADDEN G., GOODWIN R.G.;			
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).			
CC	-1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO			
CC	REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL			
CC	ANTIVIRAL EFFECTS OF THE CYTOKINE.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
DR	EMBL: M17433; -; NOT ANNOTATED_CDS.			
DR	EMBL: A23727; E159408; -.			
DR	HSSP: P19436; 11NR.			
KW	RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.			
FT	SIGNAL	1	16	POTENTIAL.
FT	CHAIN	17	325	PROTEIN T2.
FT	DOMAIN	27	186	4 X TNFR-CYS.
FT	REPEAT	27	62	TNFR-CYS 1.
FT	REPEAT	63	104	TNFR-CYS 2.
FT	REPEAT	105	147	TNFR-CYS 3.
FT	REPEAT	148	186	TNFR-CYS 4.
FT	CARBOHYD	105	105	POTENTIAL.
FT	CARBOHYD	181	181	POTENTIAL.
FT	CARBOHYD	203	203	POTENTIAL.
FT	CARBOHYD	238	238	POTENTIAL.

01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
 GN TNFR1 OR TNFR-1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9187885.
 RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
 RA WONG G.H., CHEN E.Y., GEDEDEL D.V.,
 RA PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91246168.
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.,
 RN MOL. CELL. BIOL. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91285014.
 RA BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
 RA GRAY P.W., FELDWMANN M., FOXWELL B.M.J.,
 RN EUR. J. IMMUNOL. 21:1649-1656(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE-SPLEEN.
 RX MEDLINE: 92039815.
 RA ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.,
 RN IMMUNOGENETICS 34:338-340(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94245292.
 RA BEBO B.F., LINTHICUM D.S.,
 RN IMMUNOGENETICS 39:450-451(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93156721.
 RA ROTHE J., BLUTHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.,
 RN MOL. IMMUNOL. 30:165-175(1993).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M60468; G198926; -;
 DR EMBL: M59377; G202097; -;
 DR EMBL: X59238; G53579; -;
 DR EMBL: X57796; G54849; -;
 DR EMBL: L26349; G430733; -;
 DR EMBL: M76556; G202102; -;
 DR EMBL: M88067; G202102; JOINED.
 DR EMBL: M76555; G202102; JOINED.
 DR PIR: A38634; GOMSTL.
 DR PIR: A16677; S16677.
 DR PIR: S19021; S19021.
 DR HSSP: P19438; 1TNR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR PROSITE: PS50017; DEATH_DOMAIN.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 21
 FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.
 FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 213 235 POTENTIAL.
 FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 196 4 X TNFR-CYS.
 FT REPEAT 43 82 TNFR-CYS 1.
 FT REPEAT 83 125 TNFR-CYS 2.
 FT REPEAT 126 166 TNFR-CYS 3.
 FT REPEAT 167 196 TNFR-CYS 4.
 FT DOMAIN 356 441 DEATH DOMAIN.
 FT DISULFID 44 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 81 BY SIMILARITY.
 FT DISULFID 84 99 BY SIMILARITY.

FT DISULFID 102 117 BY SIMILARITY.
 FT DISULFID 105 125 BY SIMILARITY.
 FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.
 FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 191 BY SIMILARITY.
 FT DISULFID 185 195 BY SIMILARITY.
 FT CARBOHYD 54 54 POTENTIAL.
 FT CARBOHYD 151 151 POTENTIAL.
 FT CARBOHYD 202 202 POTENTIAL.
 FT CONFLICT 394 394 R -> G (IN REF. 6).
 SQ SEQUENCE 454 AA; 50129 MW; 486EBC09 CRC32;
 Query Match 7.38; Score 221; DB 9; Length 454;
 Best Local Similarity 33.18; Pred. No. 2,726-23;
 Matches 48; Conservative 21; Mismatches 65; Indels 11; Gaps 9;
 Db 49 yvhsknscctckhkygylvsdpspgdvcrecekgftaagnylrgclscctcke 108
 QY 31 YDEETSHOLDCKCPGTYLKHCHTAK-WKTVCAPCPDHYTDSWHSDECLCSPVCKE 89
 Db 109 msqvelspcgadkdvscgkengfgqylselhfgvdcspcfnq-tvlipkeqtynvcn 167
 QY 90 LQYVK-QECNRTNHNVCCKEGS---RYL-DIEF-CLKHRSQPCPGCVQAQTPERNVTCK 143
 Db 168 -chagfflrescvcpschckkneec 191
 QY 144 RCPDGFESNETSKA-P-CRRHTNC 166
 RESULT 11
 ID TNFR1_RAT STANDARD: PRT: 461 AA.
 AC P22934;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
 GN TNFR1 OR TNFR-1.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9109841.
 RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PEIZENMAIER K.,
 RA LANTZ M., OLSSON I., HUPPMANN R., STRATOWA C., ADOLF G.R.,
 RN DNA CELL. BIOL. 9:705-715(1990).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL: M63122; G207362; -;
 DR EMBL: B36585; B36555.
 DR HSSP: P19438; 1TNR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR PROSITE: PS50017; DEATH_DOMAIN.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 21
 FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR 1.
 FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 212 234 POTENTIAL.
 FT DOMAIN 235 461 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 196 4 X TNFR-CYS.
 FT REPEAT 43 82 TNFR-CYS 1.
 FT REPEAT 83 125 TNFR-CYS 2.
 FT REPEAT 126 166 TNFR-CYS 3.
 FT REPEAT 167 196 TNFR-CYS 4.
 FT DOMAIN 363 448 DEATH DOMAIN.
 FT DISULFID 44 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 81 BY SIMILARITY.
 FT DISULFID 84 99 BY SIMILARITY.
 FT DISULFID 102 117 BY SIMILARITY.

FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 185 195 BY SIMILARITY.
FT CARBOHYD 54 54 POTENTIAL.
FT CARBOHYD 151 151 POTENTIAL.
FT CARBOHYD 201 201 POTENTIAL.
SQ SEQUENCE 461 AA; 50969 MW; 82F68B08 CRC32;

Query Match 7.3%; Score 220; DB 9; Length 461;
Best Local Similarity 33.8%; Pred. No. 4,35e-23;
Matches 49; Conservative 22; Mismatches 63; Indels 11; Gaps 10;

Db 49 yabphnsicctckhgylysdcpdpgevcvcdkgtftasqnhvrcjcktrke 108
1 ydeetsHOLLDCRPGTYLKHCHTAK-WKTYCACPDPHYTDSMHTSDECLYCSPPVCKE 89
31 ydeetsHOLLDCRPGTYLKHCHTAK-WKTYCACPDPHYTDSMHTSDECLYCSPPVCKE 89
109 mfyveispcskadmtvsgcknqfgrlysethfgcvdscpfng-tvtlpekeqntvcn 167
90 L-QYVKQCEKRNTHNVCECK--E-GRYL-EIEF-CLKHRSCPPGCGVVOAGTPERNTVCK 143
QY 168 -chagffisgncpcshcknqec 191
Db 144 RCPDGF-S-NETSSKAPCRKHTNC 166
OY 144 RCPDGF-S-NETSSKAPCRKHTNC 166

RESULT 12 STANDARD: PRT: 416 AA.
AC NGFR-CHICK
ID NGFR-CHICK
PI8519;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LINGFR)
OC GALLUS GALLUS (CHICKEN).
OC EDUAROTA; METAQOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 9016579.
RA LANGE T.H., WESSAMP G., HELDER J.C., RADEKE M.J., MISKO T.P.,
RA SHOOTER E.M., REICHARDT L.F.,
RA NEURON 2:1123-1134(1989).
RL [2]
SEQUENCE OF 21-416 FROM N.A.
MEDLINE; 90152140.
RA HEDER J.G., FATEMIE-NAINIE S., WHEELER E.F., BOTHWELL M.,
RL DEV. BIOL. 137:287-304(1990).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
PIR: JN0006; JN0006.
PIR: A60304; A60504.
DR PROSITE; PS00652; TNFR-NGFR.
DR RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KW PHOSPHORYLATION; SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 416 NGF RECEPTOR.
FT DOMAIN 29 239 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 240 261 POTENTIAL.
FT DOMAIN 262 416 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 181 4 X TNFR-CYS.
FT REPEAT 23 57 TNFR-CYS 1.
FT REPEAT 58 100 TNFR-CYS 2.

FT REPEAT 101 140 TNFR-CYS 3.
FT REPEAT 141 181 TNFR-CYS 4.
FT DOMAIN 188 236 SER/THR-RICH.
FT DOMAIN 333 410 DEATH DOMAIN.
FT DISULFID 24 35 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 39 56 BY SIMILARITY.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 78 91 BY SIMILARITY.
FT DISULFID 81 99 BY SIMILARITY.
FT DISULFID 101 114 BY SIMILARITY.
FT DISULFID 117 130 BY SIMILARITY.
FT DISULFID 120 138 BY SIMILARITY.
FT DISULFID 141 156 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT CARBOHYD 162 180 BY SIMILARITY.
FT CARBOHYD 52 52 POTENTIAL.
FT CONFLICT 36 36 C -> Y (IN REF. 2).
FT CONFLICT 173 173 T -> K (IN REF. 2).
FT CONFLICT 276 276 N -> S (IN REF. 2).
FT CONFLICT 396 396 K -> R (IN REF. 2).
SQ SEQUENCE 416 AA; 44654 MW; 4D3F086A CRC32;

Query Match 7.1%; Score 215; DB 6; Length 416;
Best Local Similarity 30.4%; Pred. No. 4,53e-22;
Matches 45; Conservative 27; Mismatches 70; Indels 6; Gaps 6;

Db 36 ckacnlgeyvvpcgvn-qvcepcldsvtsatepckpctq-cvylhmsapcve 93
41 CDKCPGTYLKHCHTAKWKTYCACPDPHY-YTDSMHTSDECLYCSPPVCKELOYKQCNR 99
QY 94 sddavccrcaygyfdealsgcsceisvevgfmlfpcrdsqdvceecpvgtfdsanf 153
QY 100 TNHNVCECKERYL-EIE-FCLKHRSCPPGCGVVOAGTPERNTVCKRCPDGFNETSSK 157
Db 154 dpcplciceeneyvke-clatsdaec 180
QY 158 APCRKHNGSVFGLLTQKGNATHDNIC 185

RESULT 13 STANDARD: PRT: 427 AA.
ID NGFR-HUMAN
AC P08138;
DT 01-AUG-1988 (REL. 08, CREATED)
DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LINGFR).
GN NGFR.
OS HOMO SAPIENS (HUMAN).
OC EDUAROTA; METAQOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87051725.
RA JOHNSON D., LANAHAN A., BUCK C.R., SERGAL A., MORGAN C., MERCER E.,
RA BOTHWELL M., CHAO M.,
RL CELL 47:545-554(1986).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
PIR: M14764; G189205; .
PIR: A25218; GQHUN.
DR HSSP; P19438; ITRN.
DR MIM; 162010; .
DR PROSITE; PS00652; TNFR-NGFR.
DR RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KW PHOSPHORYLATION; SIGNAL.

FT	SIGNAL	1	28	
FT	CHAIN	29	427	NGF RECEPTOR.
FT	DOMAIN	29	250	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	251	272	POTENTIAL.
FT	DOMAIN	273	427	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	31	189	4 X TNFR-CYS.
FT	REPEAT	31	65	TNFR-CYS 1.
FT	REPEAT	66	107	TNFR-CYS 2.
FT	REPEAT	108	147	TNFR-CYS 3.
FT	REPEAT	148	189	TNFR-CYS 4.
FT	DOMAIN	344	421	DEATH DOMAIN.
FT	DISULFID	32	43	BY SIMILARITY.
FT	DISULFID	44	57	BY SIMILARITY.
FT	DISULFID	47	64	BY SIMILARITY.
FT	DISULFID	67	83	BY SIMILARITY.
FT	DISULFID	86	99	BY SIMILARITY.
FT	DISULFID	89	107	BY SIMILARITY.
FT	DISULFID	109	122	BY SIMILARITY.
FT	DISULFID	125	138	BY SIMILARITY.
FT	DISULFID	128	146	BY SIMILARITY.
FT	DISULFID	149	164	BY SIMILARITY.
FT	DISULFID	167	180	BY SIMILARITY.
FT	DISULFID	170	188	BY SIMILARITY.
FT	DOMAIN	197	248	SER/THR-RICH.
FT	CARBOHYD	60	60	POTENTIAL.
SQ	SEQUENCE	427 AA:	45183 MW;	EE2924BD CRC32;

Query Match 7.0%; Score 213; DB 6; Length 427;
Best Local Similarity 34.9%; Pred. No. 1,156-21;
Matches 45; Conservative 19; Mismatches 60; Indels 5; Gaps 5.

Db	44	cckanlgesvapgpcan-qlvcepcldsvtsfdvvsatepekcpte-cvqlgmsapcve	101
Qy	41	cdkcpgrgylkqhcktaikwtvcapcpdhy-ytdsmhtsdecltgcspvckelqykcncnr	99
Db	102	addavrcrcaygygqdetlrcceacrcvcaagslvtscqdkqntvceecpdtgdeanhv	161
Qy	100	tnhrvceckegryl-el-efclkhrrscpgegvagiprrntvckrcpdpdfeffnrtssk	157
Db	162	dcolpctve	170
Qy	158	apcrkhtnc	166

RESULT 14
ID NGFR.RAT STANDARD: PRT: 425 AA.
AC P07174:
01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GPR80-LNGFR).
GN NGFR.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87115859.
RA RADEKE M.J., MISKO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M.;
RA NATURE 325:593-597(1987).
RN [2]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE; 93077038.
RL METSIS R., TIMMUSK T., ALLIKMETS R., SAARMA M., PERSSON H.;
RL GENE 121:247-254(1992).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

Query Match	Best Local Similarity	Score	DB	Length
Matches	43; Conservative	21; Mismatches	60; Indels	5; Gaps
Db 45	ckachlgsgvqgpcgan-qlycepcldvtsdvssatepckpcte-clglgmsapcve	102		
Qy 41	CDKPPGTYLKHOCITAKKVTVCAPCPDHY-YTDSWHTSDECLYSPCKELQYVKOCNR	99		
Db 103	addavcraaygygdeeghceascvcsyglvtsqdkngtccespctgdeanhv	162		
Qy 100	TNHRVCECKEGRIEIE--FLKHRSCEPPGGVQAGIPERNIVCKKCPDGFSSNETSSK	157		
Db 163	dpcldpctvc	171		
Qy 158	APCRKHTNC	166		
RESULT 15				
ID	FASA_BOVIN	STANDARD:	PRG:	323 AA.
AC	P51867:			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)			
DE	(APO-1 ANTIGEN) (CD95).			
GN	APLI OR FAS.			
OS	BOS TAURUS (BOVINE).			
OC	EUKARYOTA, METAZOIA, CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:			
OC	EUTHERIA: ARTIODACTYLA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE: 96226401.			
RA	YOO J., STONE R.T., BEATTIE C.W.:			
RL	DNA CELL BIOL. 15:227-234(1996).			
CC	-I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MEDIATES CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE			

